



SEQUENCE LISTING

<110> Farwick, Mike

Huthmacher, Klaus

Marx, Achim

Pfefferle, Walter

<120> New Nucleotide Sequences Which Code for the menE Gene

<130> 21123/280112

<140> 09/834,722

<141> 2001-04-16

<160> 4

<170> PatentIn version 3.0

<210> 1

<211> 1570

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (230)..(1357)

<400> 1
ttcgttgcca tagacatgct ctctgcagca ctgtttgcg acgtctctc cgcatcttt 60
gtcaccaaca atggttgga actcaccggc gcaatcggcg ctggcgcgct gcttctcatc 120
gcagttggcg caggtgcatg gagcatcgac ggggttctgg caaacgcaa ggctaaatc 180
tagcgccaca actccgaatt ctgaaccatc ggactagaa tctcggaat atg aat act 238
Met Asn Thr

cgc gtc ctc gaa gca cta cct gtt gat ctt gca gat ccc acc gca att	286
Arg Val Leu Glu Ala Leu Pro Val Asp Leu Ala Asp Pro Thr Ala Ile	
5 10 15	
ctg gga gat ctc gag gac gca atc tct ggg aag aaa act ttc ctc ccc	334
Leu Gly Asp Leu Glu Asp Ala Ile Ser Gly Lys Lys Thr Phe Leu Pro	
20 25 30 35	
atc cct gta caa gat aaa acc cgt gca cag ttg ctg cgc gat tct caa	382
Ile Pro Val Gln Asp Lys Thr Arg Ala Gln Leu Leu Arg Asp Ser Gln	
40 45 50	
cga gtt ggc ctc gcc atc gat cct tgc atc gct ttg gtg atg gcc act	430
Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala Thr	
55 60 65	
tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg aat	478
Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu Asn	
70 75 80	
ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa ggc	526
Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu Gly	
85 90 95	
cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag gtg	574
Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln Val	
100 105 110 115	
ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat ctc	622
Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp Leu	
120 125 130	
agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa ctg	670
Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu Leu	
135 140 145	
aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag tta	718
Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln Leu	
150 155 160	
ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt ttt	766
Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu Phe	
165 170 175	
gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga att	814
Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg Ile	
180 185 190 195	
tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc tca	862
Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser Ser	
200 205 210	
gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc gcg	910
Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly Ala	
215 220 225	

aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg att	958
Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met Ile	
230 235 240	
gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac gag	1006
Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn Glu	
245 250 255	
ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att ctc	1054
Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile Leu	
260 265 270 275	
acc gtg act ggt cgc gtg gat acc gtc att gat tcc ggt gga ttg aag	1102
Thr Val Thr Gly Arg Val Asp Thr Val Ile Asp Ser Gly Gly Leu Lys	
280 285 290	
ttg cac cca gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc	1150
Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val	
295 300 305	
acc gcg gcg tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca	1198
Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala	
310 315 320	
att gtg gcc gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa	1246
Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu	
325 330 335	
ggc ctc gac gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat	1294
Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His	
340 345 350 355	
ctg gaa tct ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct	1342
Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala	
360 365 370	
atc gcg aag ctg ttt tagtcttcat tcttgctggc tgcaactagt ttgcccacat	1397
Ile Ala Lys Leu Phe	
375	
cttcacgggt gtacactttg gcgatctgct catcatttcc acccatgagg gtgttgccaa	1457
caactagtgc tcccacttgg gtggtgggca cgacagcgaa gtgtcggggc tgagcgtaga	1517
cctggcgaat aggggtgatca gagcgcagtg cgcaggcatg cagccatacg tca	1570
<210> 2	
<211> 376	
<212> PRT	
<213> Corynebacterium glutamicum	

<400> 2

Met Asn Thr Arg Val Leu Glu Ala Leu Pro Val Asp Leu Ala Asp Pro
 1 5 10 15

Thr Ala Ile Leu Gly Asp Leu Glu Asp Ala Ile Ser Gly Lys Lys Thr
 20 25 30

Phe Leu Pro Ile Pro Val Gln Asp Lys Thr Arg Ala Gln Leu Leu Arg
 35 40 45

Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val
 50 55 60

Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr
 65 70 75 80

Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly
 85 90 95

Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly
 100 105 110

Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala
 115 120 125

Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala
 130 135 140

Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro
 145 150 155 160

Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu
 165 170 175

Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln
 180 185 190

Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr
 195 200 205

Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile
 210 215 220

Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly
 225 230 235 240

Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe
 245 250 255

Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp
 260 265 270

Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Val Ile Asp Ser Gly
 275 280 285

Gly Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile
 290 295 300

Lys Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu
 305 310 315 320

Gly Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu
 325 330 335

Val Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg
 340 345 350

Leu Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp
 355 360 365

Arg Arg Ala Ile Ala Lys Leu Phe
 370 375

<210> 3

<211> 19

<212> DNA

<213> PCR primer

<400> 3

ctcactccgt tgaatttg

<210> 4

<211> 19

<212> DNA

<213> PCR primer

<400> 4

caggtgcatt tctgtagcc